



REPLACEMENT SHEET  
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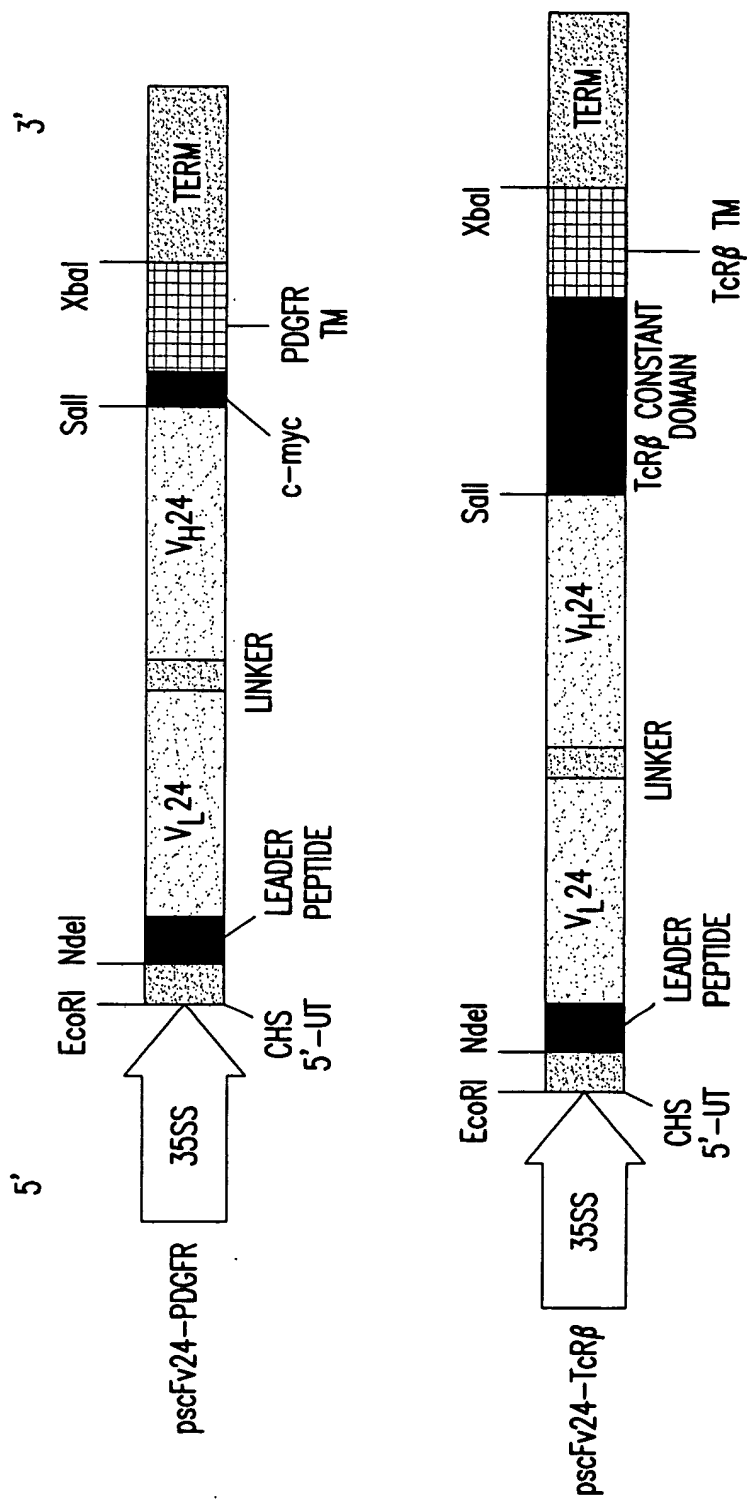


FIG.2



REPLACEMENT SHEET

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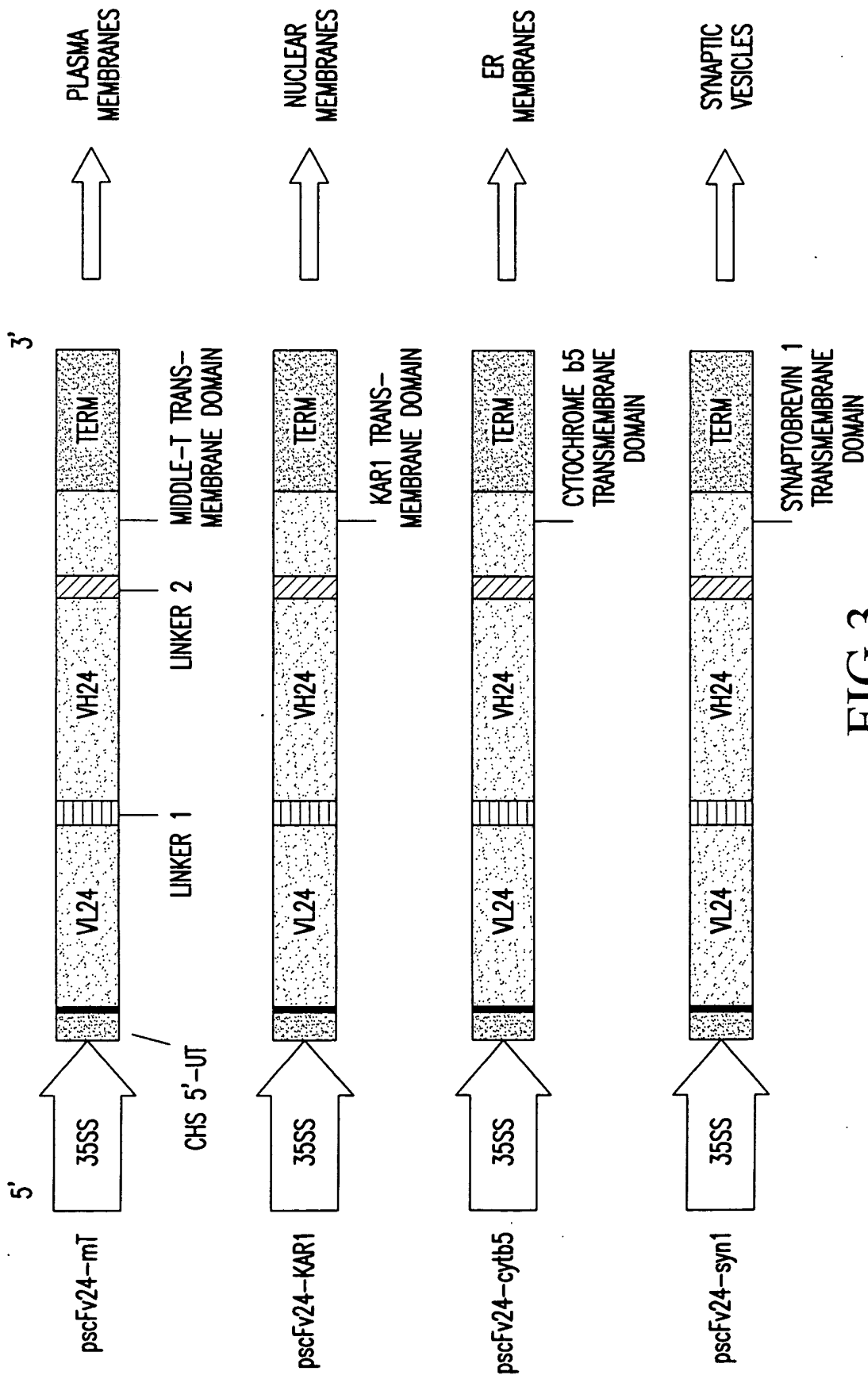


FIG.3

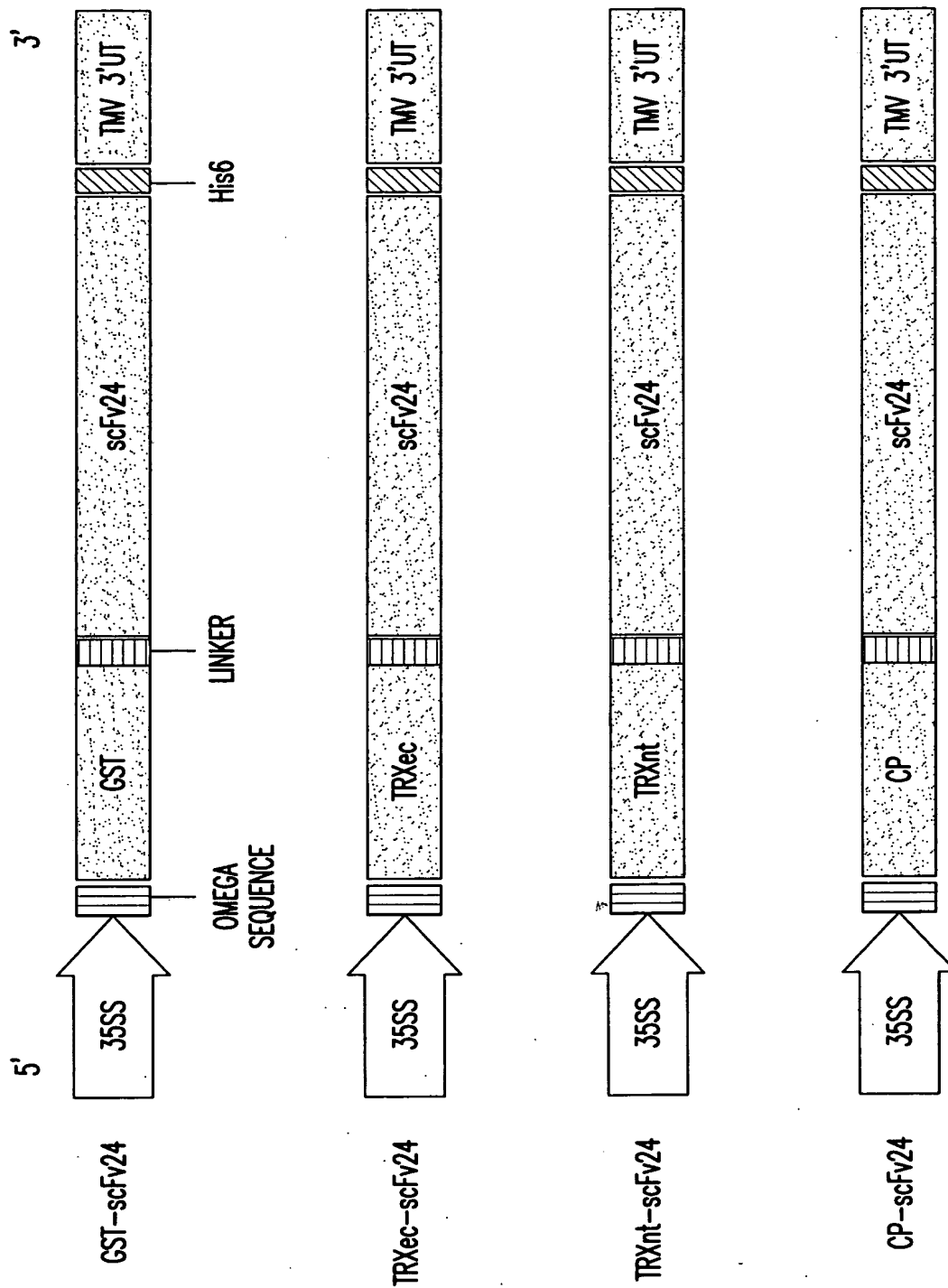
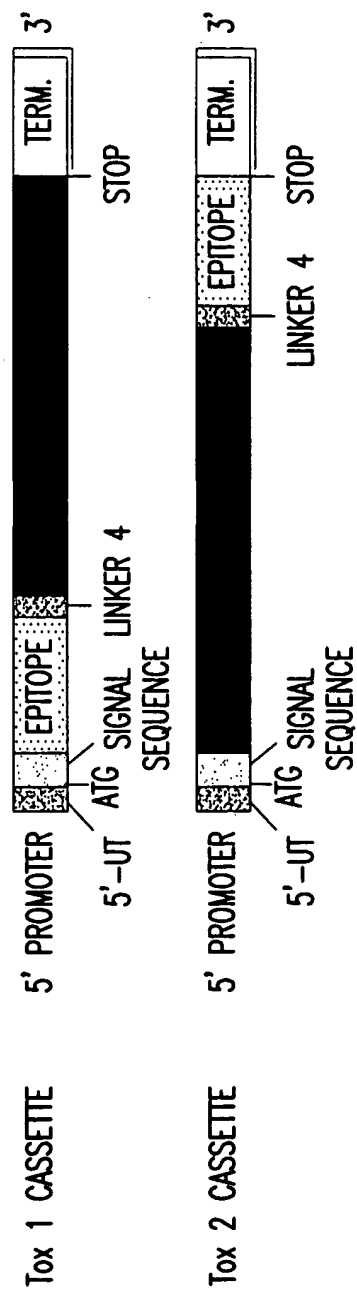
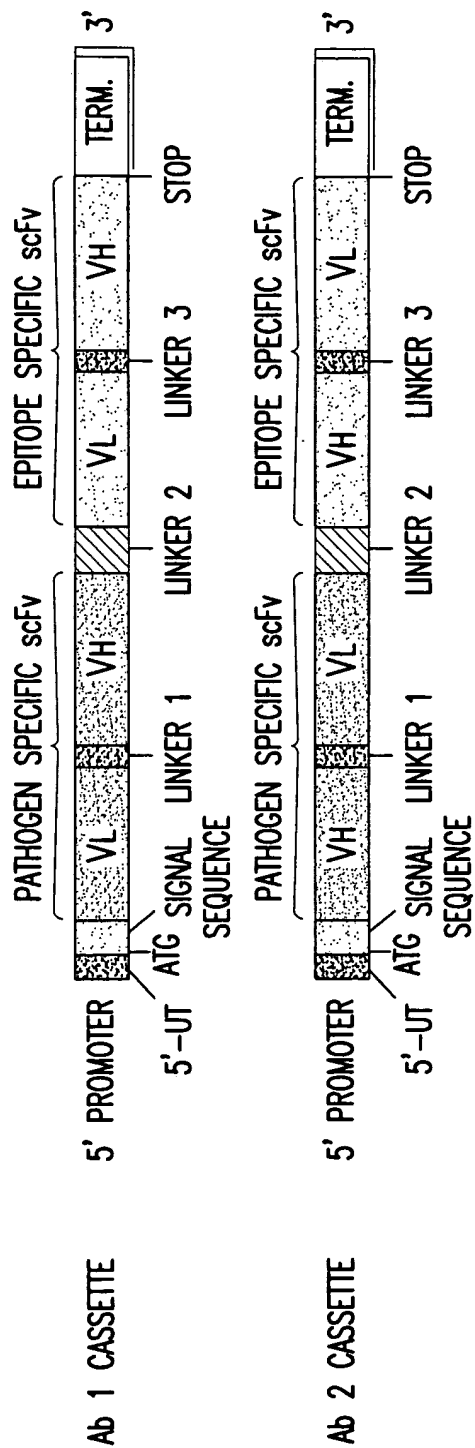
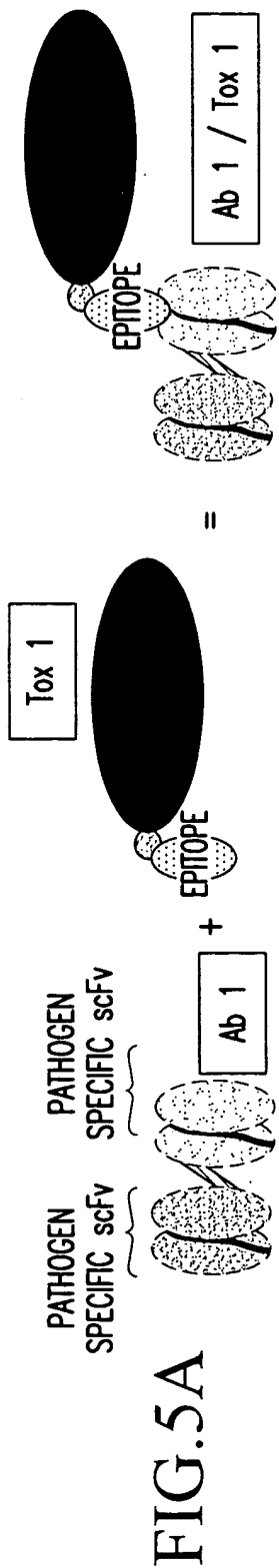


FIG.4

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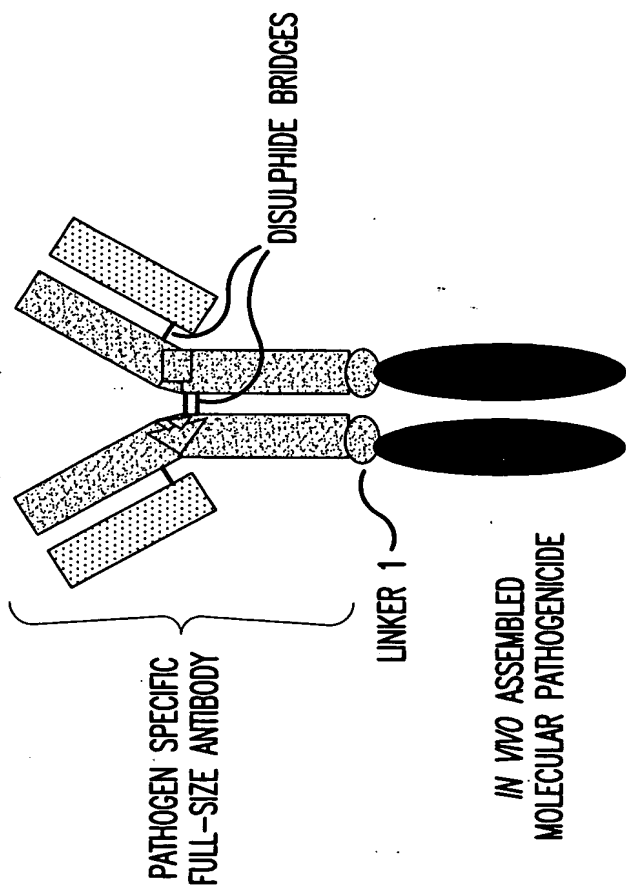


FIG.6A

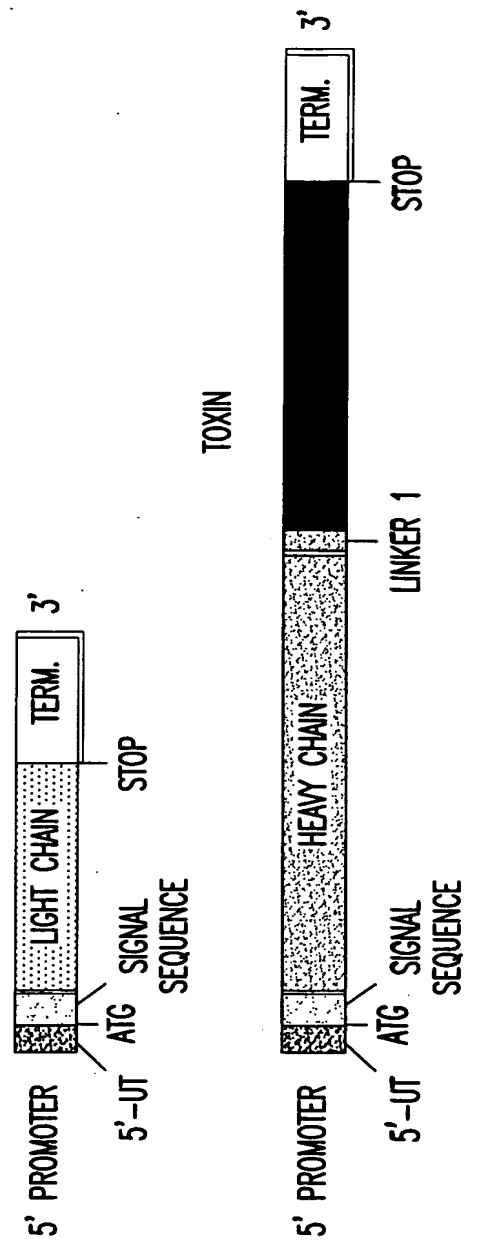
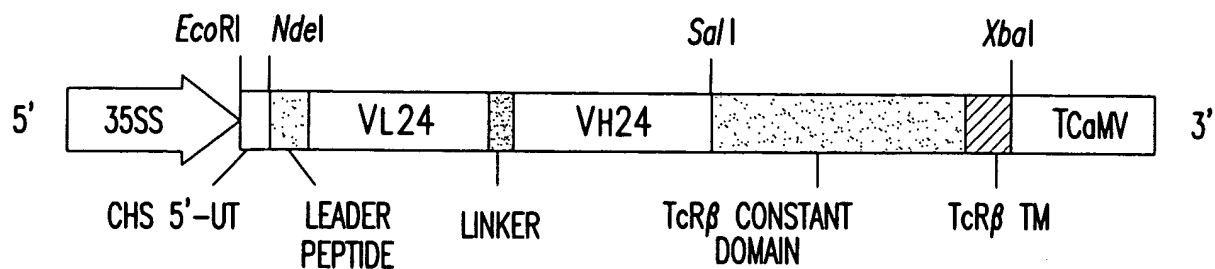


FIG.6B

# REPLACEMENT SHEET

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*pscFv24-TcRβ*

FIG.7

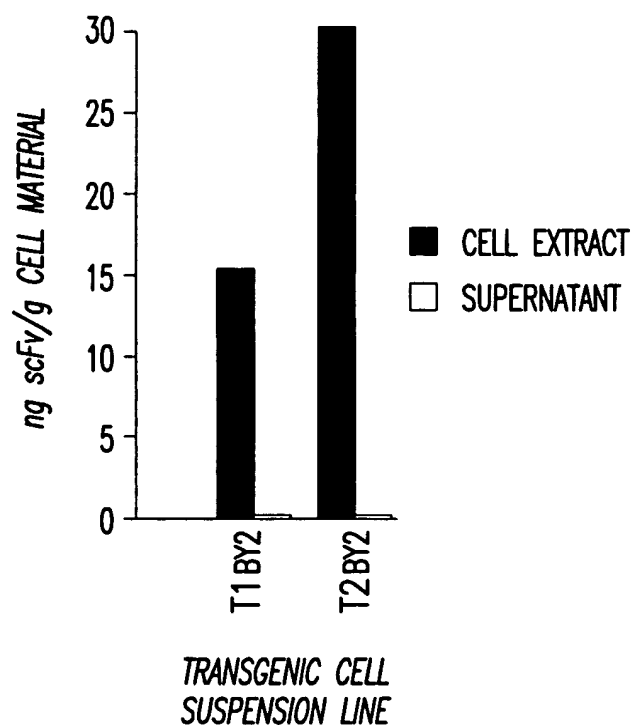


FIG.8

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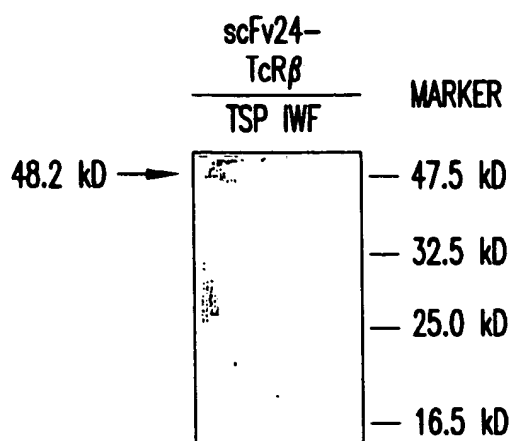


FIG.9



FIG.10A

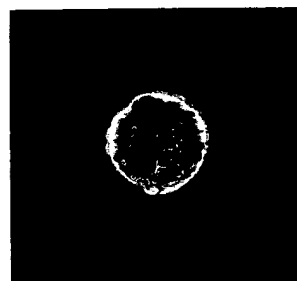


FIG.10B

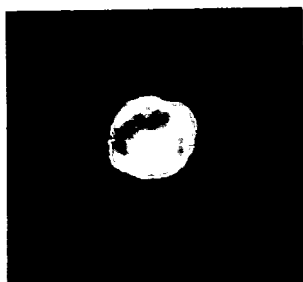


FIG.10C

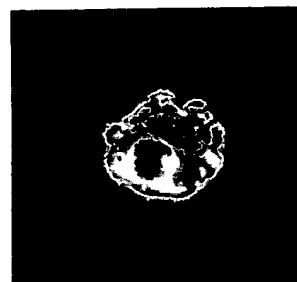


FIG.10D



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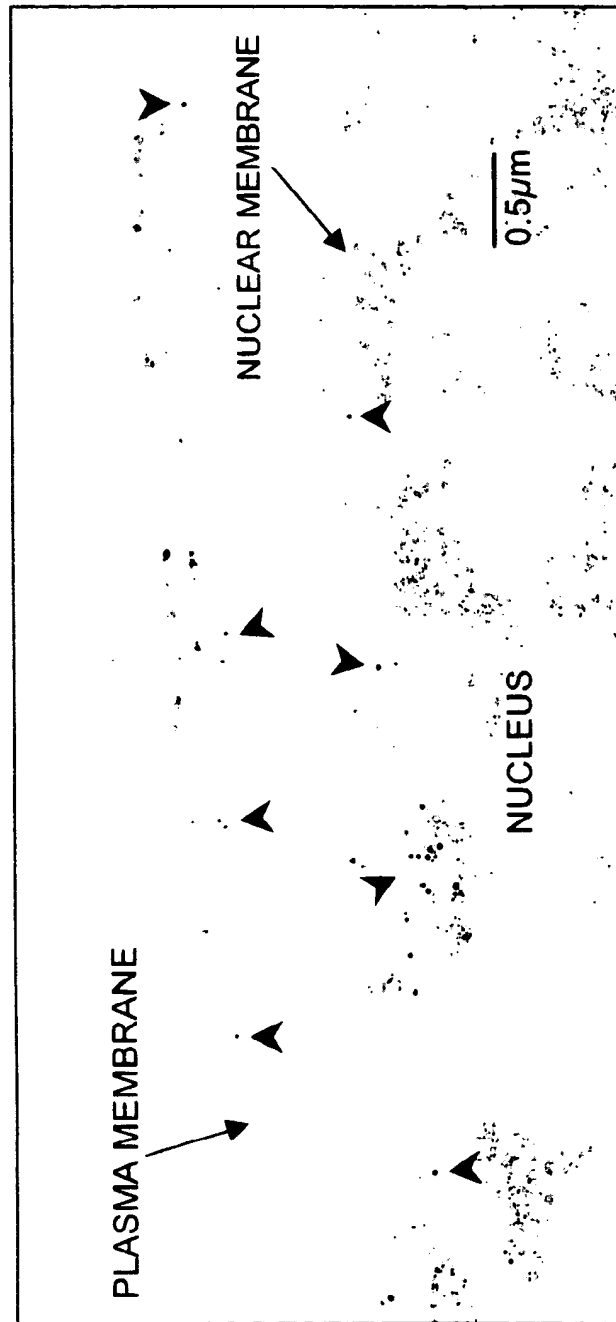


FIG.11

# REPLACEMENT SHEET

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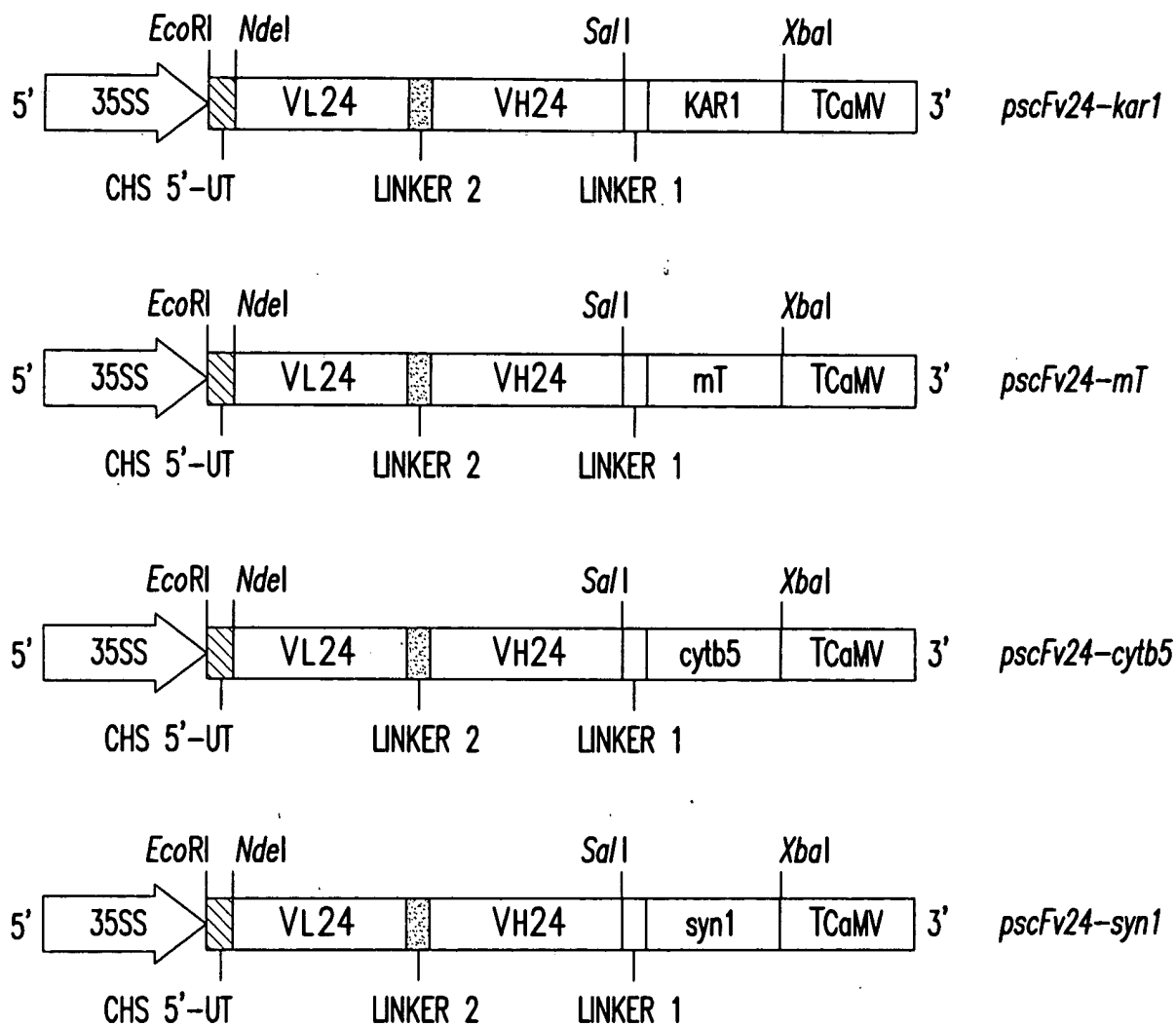


FIG.12A

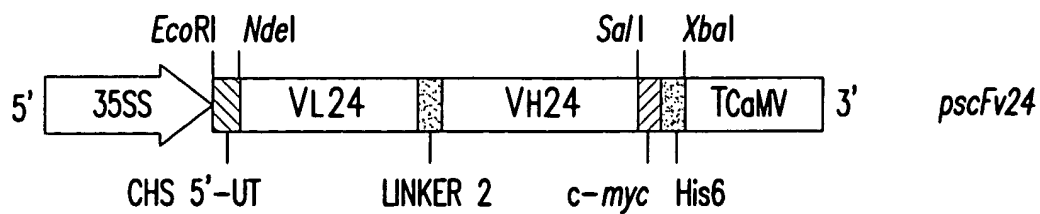
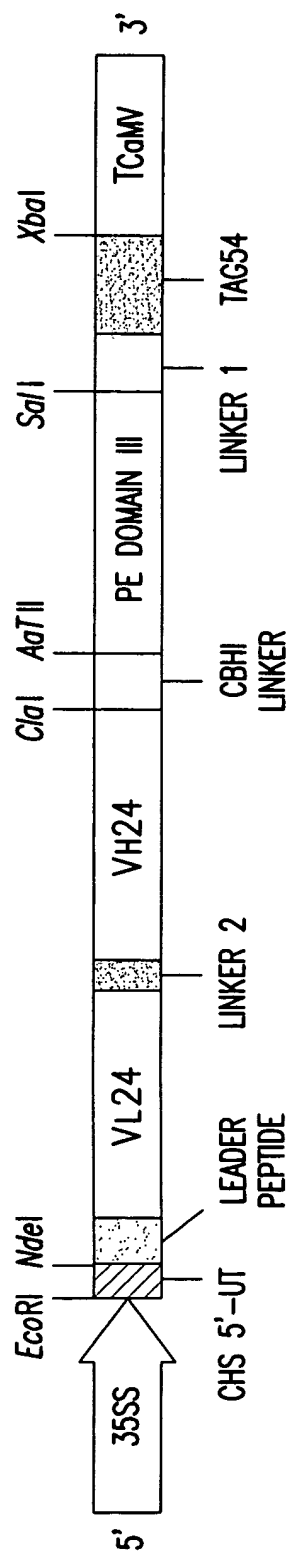


FIG.12B



*pscFv24-PE400*

FIG.13

# REPLACEMENT SHEET

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scFv24 MQIVLTQSPA IMSASPGEKV TMTCSASSSV SKMQWYQQKS GTSPKRWIYD  
 Framework I CDR LI Framework II

scFv24 TSKLASGVPG RFSGSGSGTS YSLTISSMEA EDAATYYCQQ WSSNPLTFGA  
 CDR LII Framework III CDR LIII

scFv24 GTKLEIKGST SGSGKSSEGG GEVQLQQSGP ELVNPASVK MSCKASGYTF  
 Framework IV Linker 212 Framework I

scFv24 ITYVMHVKQ KPGQGLEWIG YINPNKDGTK FNEKFKGKAT LTSDKSSNTA  
 CDR LI Framework II CDR LII Framework III

scFv24 YMELSSLTSE DSAVYYCARD YDYDWFAYWG QGTLVTVSAV DGGGSMKRML  
 Framework III CDR LIII Framework IV Linker RNase

RnaseE INATQQEELR VALVDGQRLY DLDIESPGHE QKKANIYKKGK ITRIEPSLEA  
*E. coli* RNase E gene --->

RnaseE AFVDYGAERH GFLPLKEIAR EYFPANYSAH GRPNIKDVL R EGQEVIVQID

RnaseE KEERGNKGAA LTFISLAGS YVLMPNNPR AGGISRRIEG DDRTELKEAL

RnaseE ASLELPEGMG LIVRTAGVGK SAEALQWDLS FRLKHWEAIK KAAESRPAPF

RnaseE LIHQESNVIV RAFRDYLRQD IGEILIDNPK VLELARQHIA ALGRPDFSSK

RnaseE IKLYTGEIPL FSHYQIESQI ESAFQREVRL PSGGSIVIDS TEALTAIDIN

RnaseE SARATRGGDI EETAFTNTLE AAEIARQLR LRDLGGLIVI DFIDMTPVRH

RnaseE QRAVENRLRE AVRQDRARIQ ISHISRFGLL EMSRHRSPS LGESSHHVCP

RnaseE RCGTGTVRD NESLSLSILR LIEEEALKEN TQEVHAIVPV PIASYLLNEK

RnaseE RSAVNAIETR QDGVRCVIVP NDQMETPHYH VVRVRKGEET PTLSYMLPKL

RnaseE HEEAMALPSE EEFAERKRPE QPALATFAMP DVPPAPTPAE PAAPVVAPAP

RnaseE KAAPATPAAP AQPGLLSRFF GALKALFSGG EETKPTEQPA PKAEAKPERQ

RnaseE QDRRKPRQNN RRDRNERRDT RSERTEGSDN REENRRNRRQ AQQQTAETRE

RnaseE SRQQAQVTEK ARTADEQQAP RRERSRRRND DKRQAQQEAK ALNVEEQSVQ

RnaseE ETEQEERVRP VQPRRKQRQL NQKVRYEQSV AEEAVVAPVV EETVAAEPIV

RnaseE QEAPAPRTEL VKVPLPVVAQ TAPEQQEENN ADNDRDNGGMP SFSPLASSPA

RnaseE RKWSASSSL S

FIG.14

# REPLACEMENT SHEET

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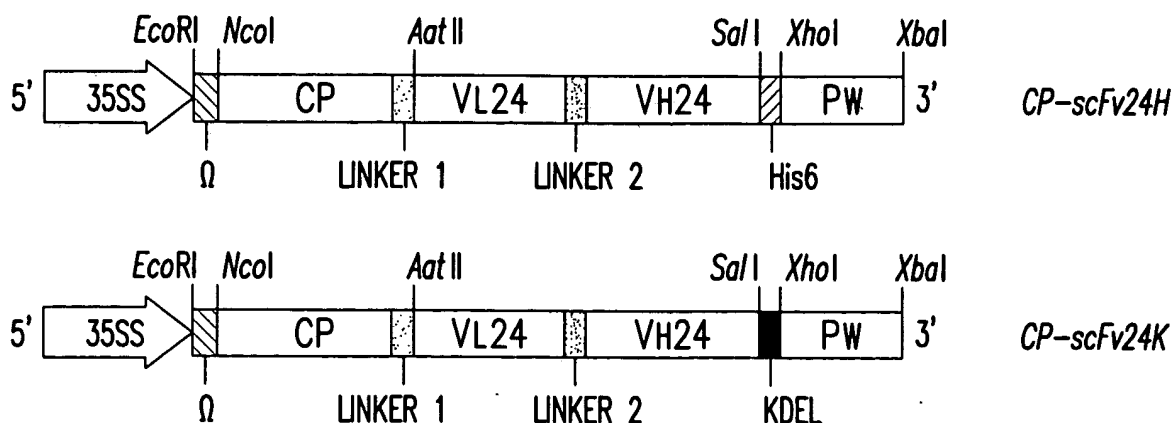


FIG.15A

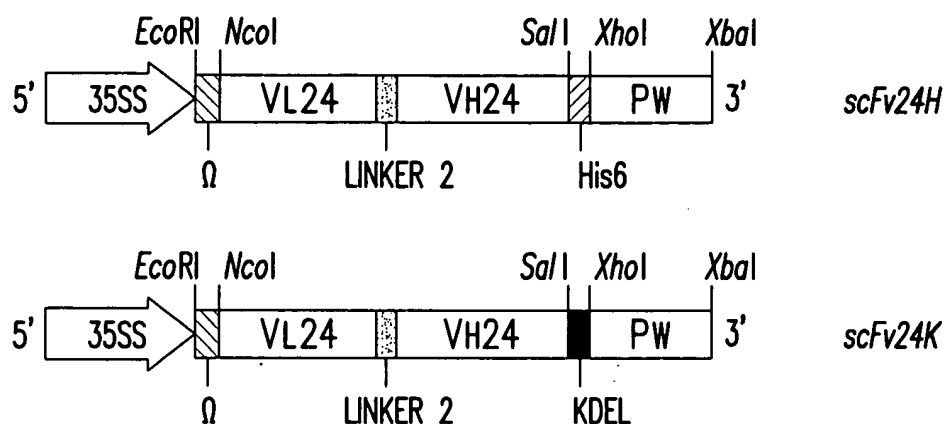


FIG.15B

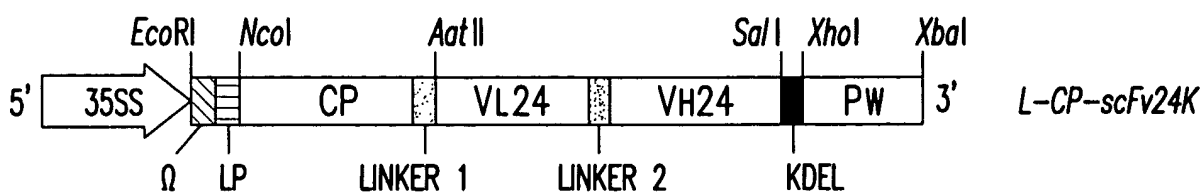


FIG.15C

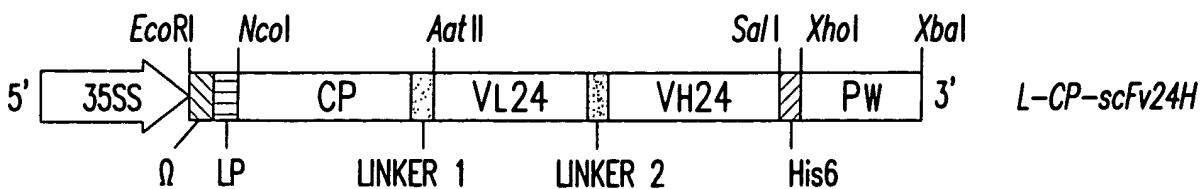


FIG.15D

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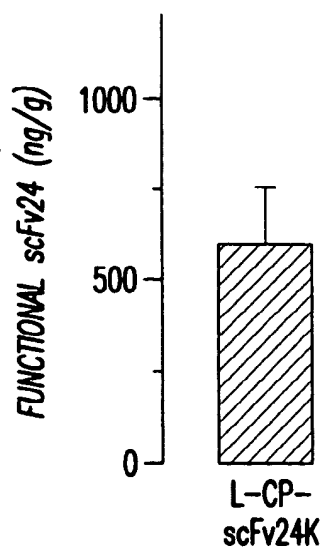


FIG.16

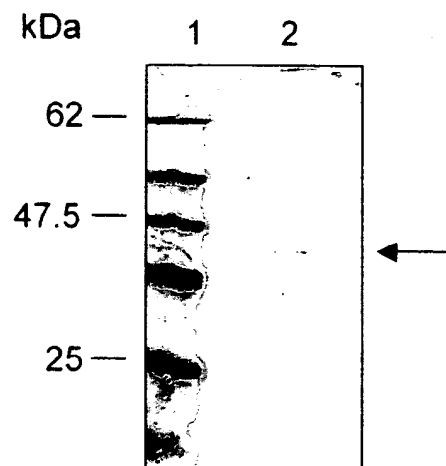


FIG.17

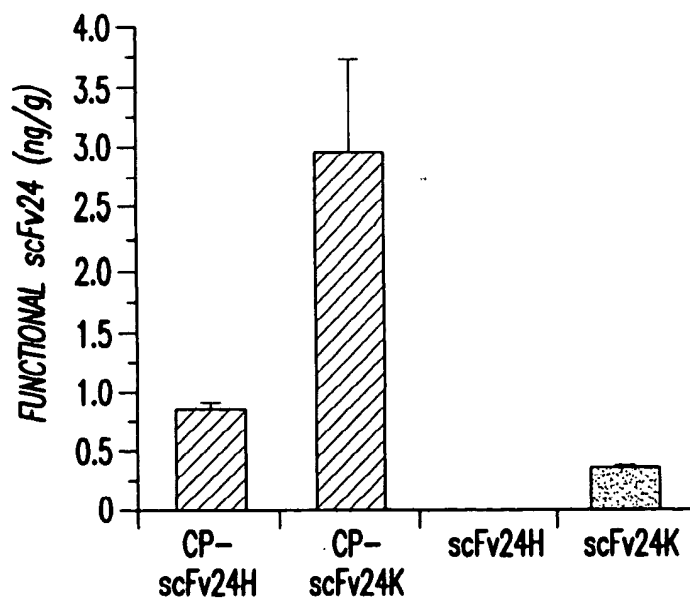


FIG.18

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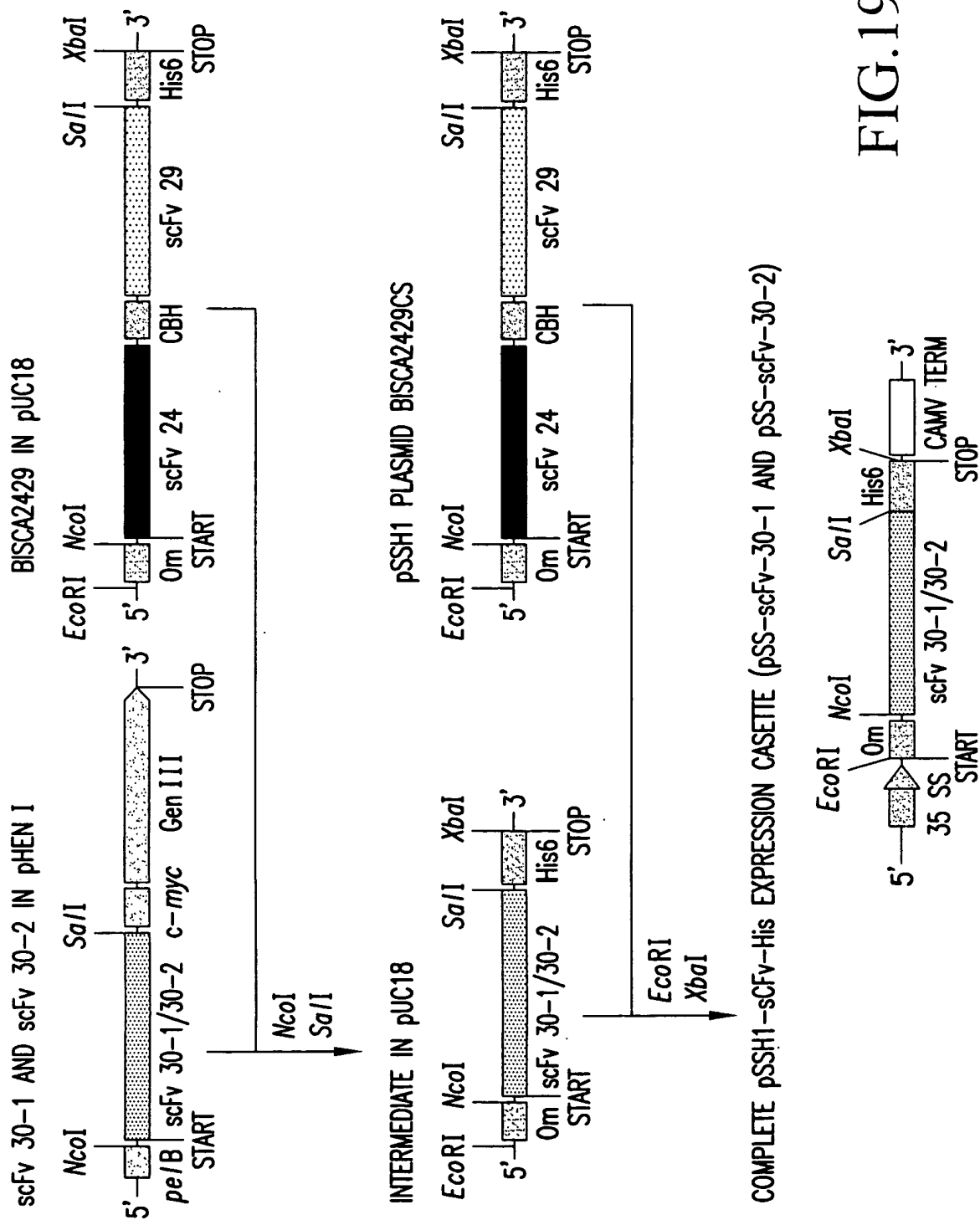
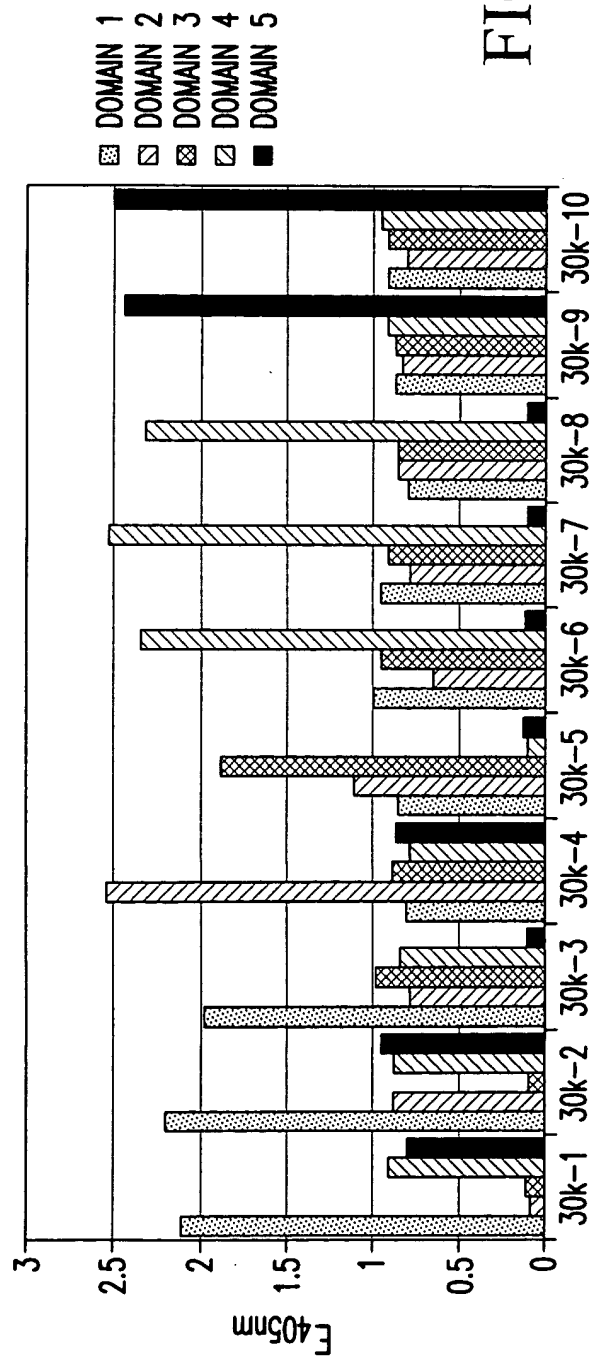
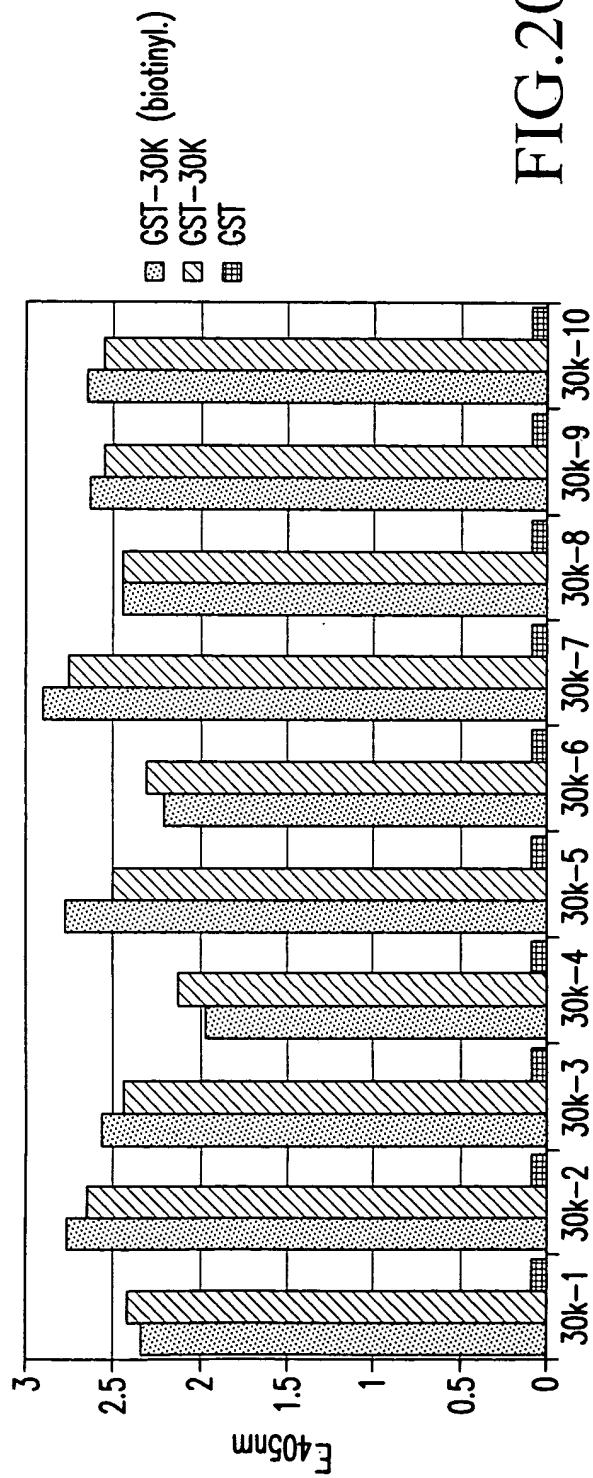


FIG.19





|           |               |              |  |               |              |
|-----------|---------------|--------------|--|---------------|--------------|
| scFv 30-1 | --EVHCKQSG    | AELVKPGASV   | KLSCRASDYT                                 | FTSYMYMWVK    | QRPQGQGLEWI  |
| scFv 30-2 | --EVKLQQSG    | AELVKPGASV   | KISCKASDYS                                 | FTGYNMNMWVK   | QSHGKSLEWI   |
|           |               |              | Framework I                                | CDR H1        | Framework II |
| scFv 30-1 | GEIKPSGNGI    | NENEKFKSKA   | TLTSDYSSST                                 | AYMQLSSLTS    | EDSAVYYCTR   |
| scFv 30-2 | GNINPYYGSI    | SYNQKFKGKA   | TLTVDKSSST                                 | AYMQLNSLTS    | EDSAVYYCAV   |
|           |               | CDR HII      |  | Framework III |              |
| scFv 30-1 | SGNAMD---     | Y            | WGQGTTVT                                   | VS            | SGGGSGGGGG   |
| scFv 30-2 | GGNYVDWFAY    |              | WGQGTTLVT                                  | VS            | SGGGSGGGGG   |
|           | CDR HIII      | Framework IV | Linker (Gly <sub>4</sub> Ser) <sub>3</sub> |               |              |
| scFv 30-1 | PGDRVSLSCR    | ASQISNFLH    | ----                                       | WYQQK         | SHESPRLLIK   |
| scFv 30-2 | LGDHASISCR    | SSQSLVHSNG   | NTYLHWYLN                                  | PGQSPKLLIY    | YTSQSI       |
|           | Framework I   | CDR LI       | Framework II                               | CDR LII       | SGIP         |
| scFv 30-1 | STFSGSGSGT    | DFTLSINSVD   | TEDFGMVFCQ                                 | QSNWPHRF      | FG           |
| scFv 30-2 | DRFSGSGSGT    | DFTLKISRVE   | AEDLGVYFCS                                 | QSTHVPYT      | FG           |
|           | Framework III |              | CDR LIII                                   | Framework IV  |              |
| scFv 30-1 | VDAAAEQKLI    | SEEDLNGAA*   |  |               |              |
| scFv 30-2 | VDAAAEQKLI    | SEEDLNGAA*   |  |               |              |
|           |               | c-myc tag    |  |               |              |

FIG.21

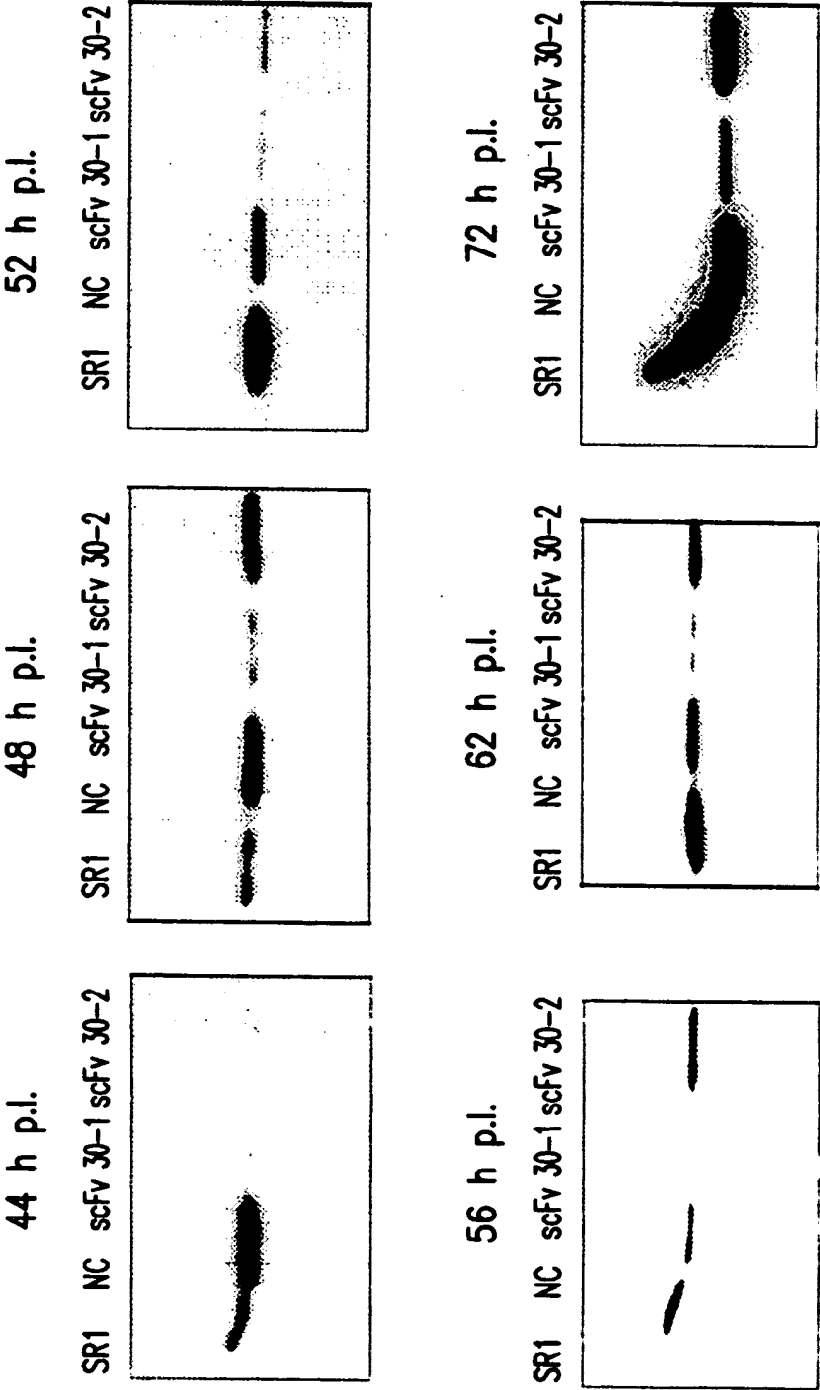


FIG.22

## REPLACEMENT SHEET

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MAEVQLQQSG AELVKPGASV KMSCKASGYT FTNYNMHWVK QTPGQGLEWI  
GAIYPRNGDT SYNQKFKGKA TLTADKSSST AYMQLSSLTS EDSAVYYCAR  
PDVWGAGTLL TVSAGAGPTS GSGKPGPEG STKGAPDVLMTQAPLTLSVT  
IGQPASISCK SSQSLLDGDG KTYLNWLLQR PGQSPKRLIY LYSKLDGVP  
DRFTGSGSGT DFTLKISRVE AEDLGVYYCW QGTHFPHTFG GGTKLEIKRA  
RAVDAAA

AMINOACID SEQUENCE OF scFv-3a-2 DERIVED FROM cDNA

### FIG.23A

MAQVTLKESG PGILKPSQTL SLTCSFSGFS LSTSGMGVGW IRQPSGKGLE  
WLAHIWDDDD KYYNPSLRSQ LTISKDTSRN QVFLRITNVD TADTATYYCA  
RGGYGNDSFP AYWGQGTLT VSSGAGPTSG SGKPGPEGSTKGAPDIVLS  
QSPKFMSTSV GDRVSITCKA SQIVRTAVAW FQKPGQSPK ALIYLASNRH  
TGVDPDRFTG GSGTDFTLTI SNVQSEDLAD YFCLQHWNYPTFTGSGTKLE  
IKRAVDAAA

AMINOACID SEQUENCE OF scFv 54-1 DERIVED FROM cDNA

### FIG.23B

MAQIQLVQSG PELKKPGQTV KISCKASAYT FTDYSMHWVK QAPGKGLKWM  
GWINTETGEP TYADDFKGRF AFSLETSAST AYLQINTLKN EDSATYFCAR  
GSGFNPYWGQ GTLVTVSAGA GPTSGSGKPG PEGSTKGAP DIVLSQSPSS  
LAVSVGEKVT MSCKSSQSLL YSSNQKNYLA WYQQKPGQSP KLLIYWASTR  
ESGVPDRFTG GSGTDFTLT INSVKAEDLA VYYCQQYYSY VTFGAGTKLE  
IKRAVDAAA

AMINOACID SEQUENCE OF scFv-3min DERIVED FROM cDNA

### FIG.23C

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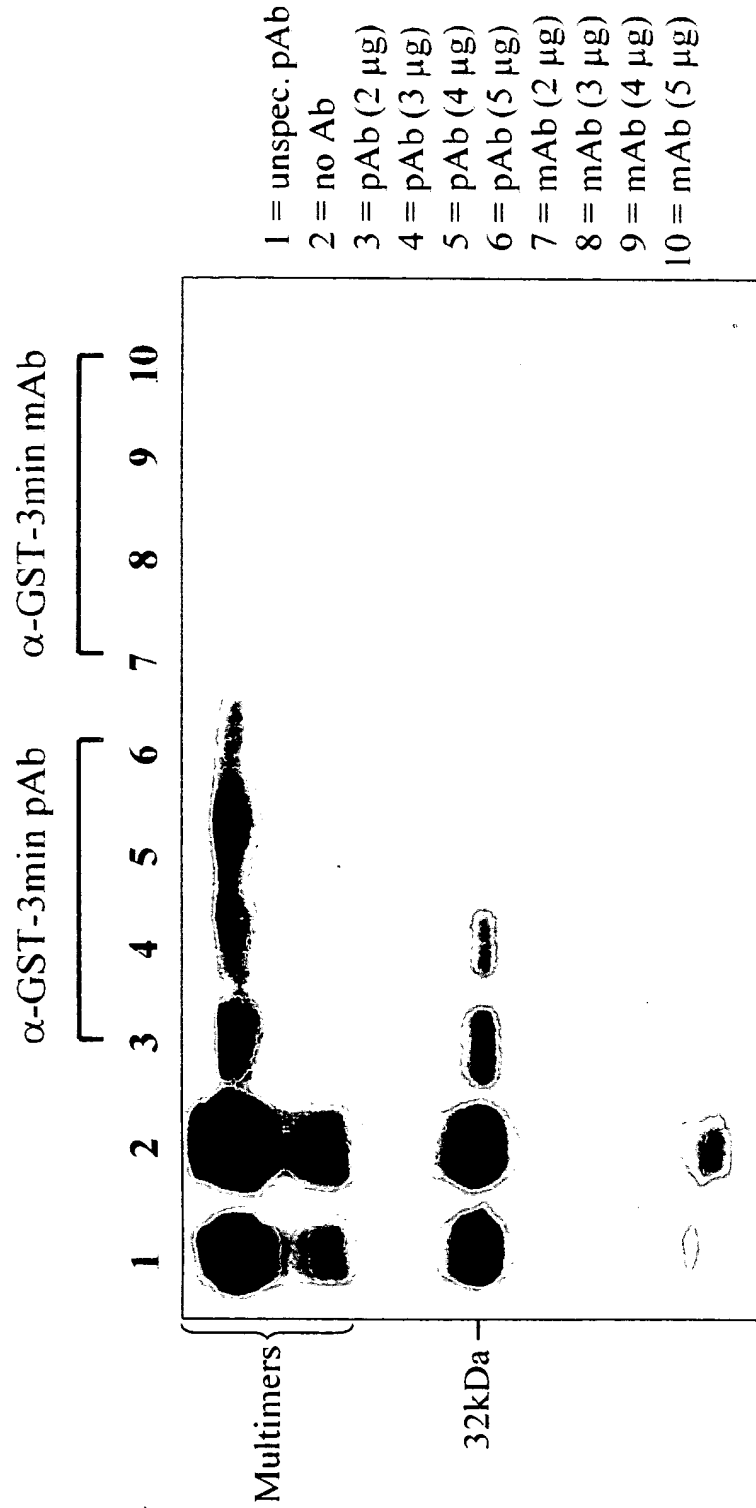


FIG.24

# REPLACEMENT SHEET

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(a) TMV-coatprotein: 127 128 129 130 131 132 133 134 135 136 137 138  
N L I V E L I R G T G S

## pVIII 9aa:

A1: K T D L VC R A T  
A2: R I V I C G R R V T T  
A4: R G T L PA R R G T T  
A5: F L R V G R Q R R D T T Q S  
B5: V V D A L G R R E T T  
C4: V A G M L G AN K R G T T  
D5: R P W E L L GT R R S E T  
E5: P S A L L GT R R S E T  
F3: K N D L VS R R A E T  
G1: Q I V S A W R E T

## pVIII 9aa.Cvs:

B9/G1: C A L PA R H I R S R C  
F3: C C Q L PA R R A E T S S C  
H1: C I T S Q C R R E T T G W C  
H5: C S T T C R R S T T G  
H10: C S T T L YK R G T C

consensus-sequence: R V D L PA R E T

(b) 54K-protein: 402 403 404 405 406 407 408 409 410 411 412 413  
K H I K D W E H L E E F

A2/A9/B8/C9: K R K D G E H W L  
A6/B5/F8/H1: R Q A K S W S S L  
G5: Y Q A K E W S N L  
H10: K D W E H R V P S

consensus-sequence: K D W E/S H L

(c) GST-3min: -6 -5 -4 -3 -2 -1 +1 +2 +3 +4 +5 +6  
P K S D P Q M G K R R R

## pVIII 9aa:

A8: H P R P Q L A S L  
C2: R H P D P Q S S H S  
E7: F T D P Q L H P Q  
F5: K Q D P Q Q L Q K Q  
F8: V P D S Q Q L E W P  
G7: H C D P Q Q L Y Q R  
H1: F K D P Q Q M F R R H C  
H5: F K D G Q L R P Q

## pVIII 9aa.Cys:

A4: C P D P Q L R L H R C  
A5: C P D P Q L N S L T R C  
A7/B10/H4: C P D P Q L S S L H R C  
A8: C P D P Q L R T L H R C  
A9: C P D P Q L T S L H R C  
G4: C P D P Q L S S L H R C  
H6: C P D A Q L S G T R C

consensus-sequence: H P D P Q L S L H R

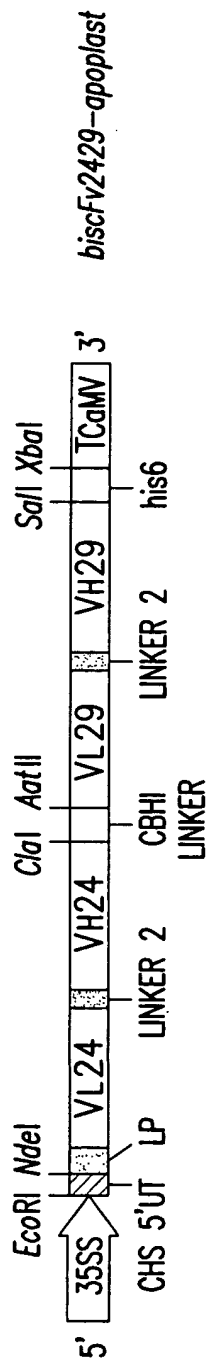


FIG. 26A

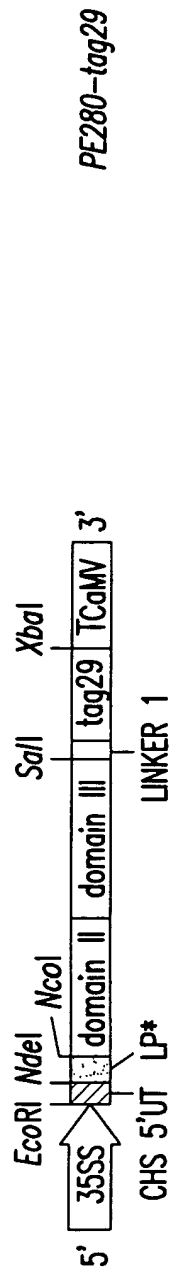


FIG. 26B

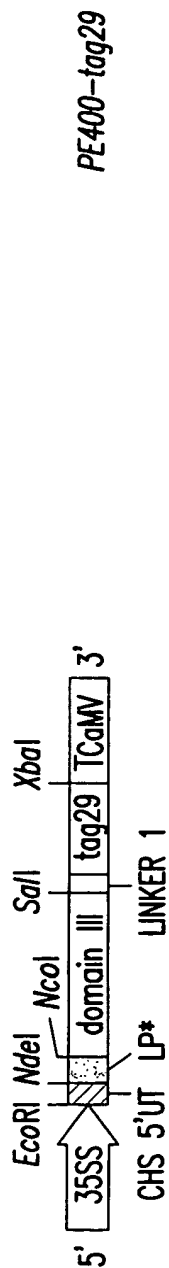


FIG. 26C



FIG. 26D

REPLACEMENT SHEET

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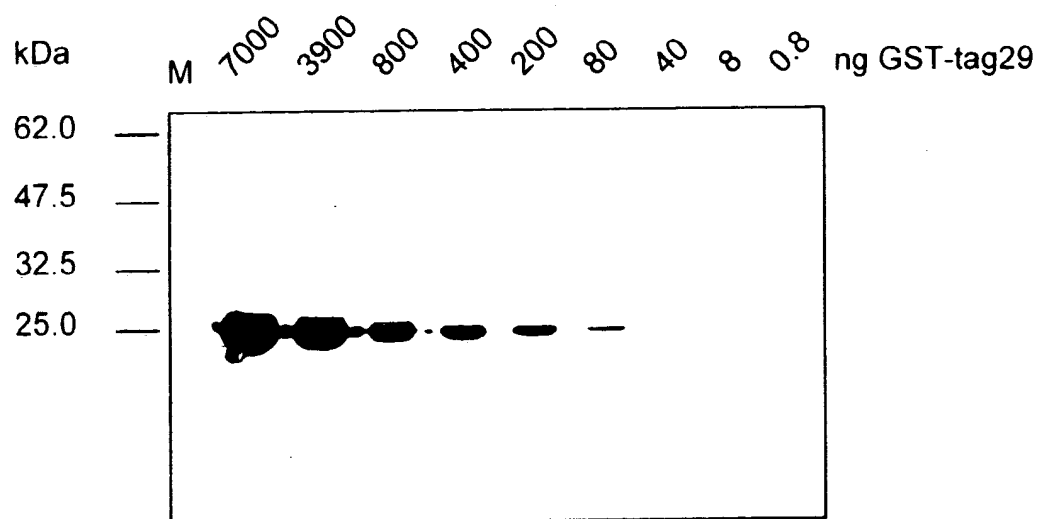


FIG.27A

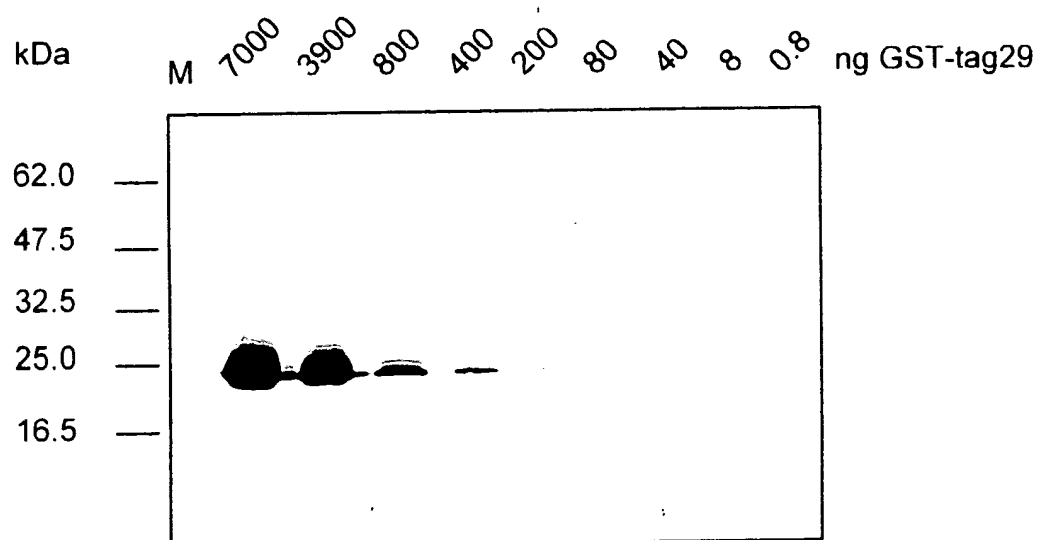


FIG.27B

# REPLACEMENT SHEET

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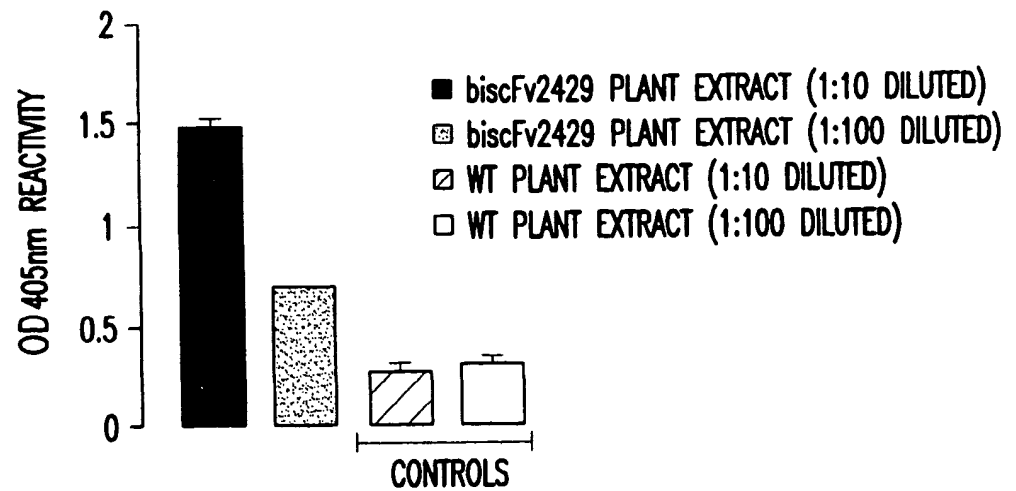


FIG.28

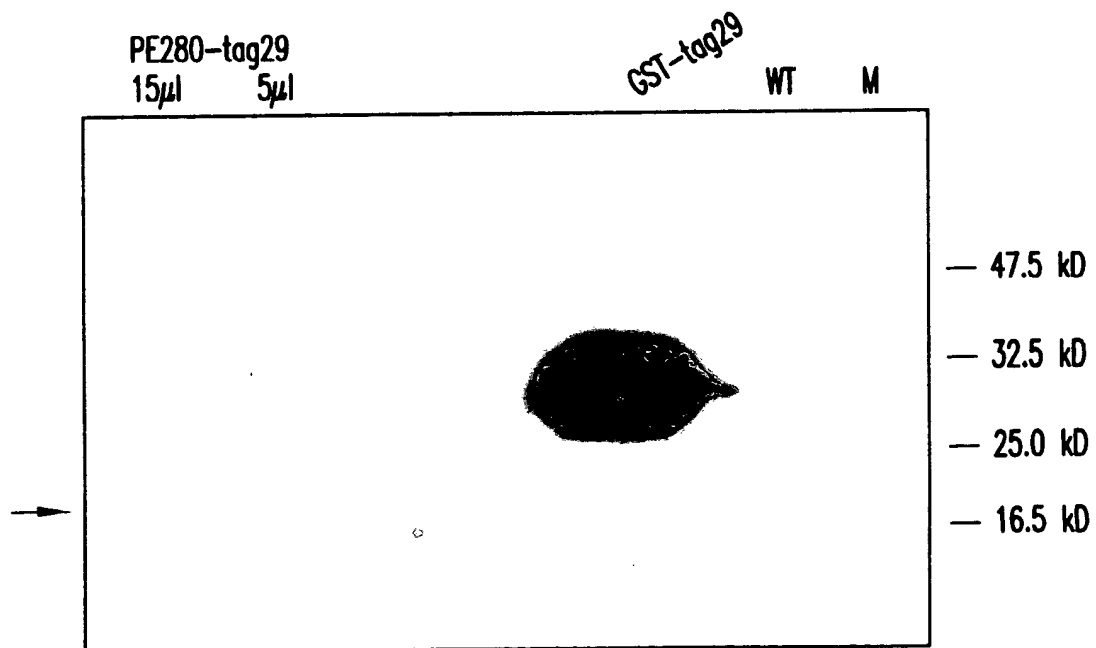
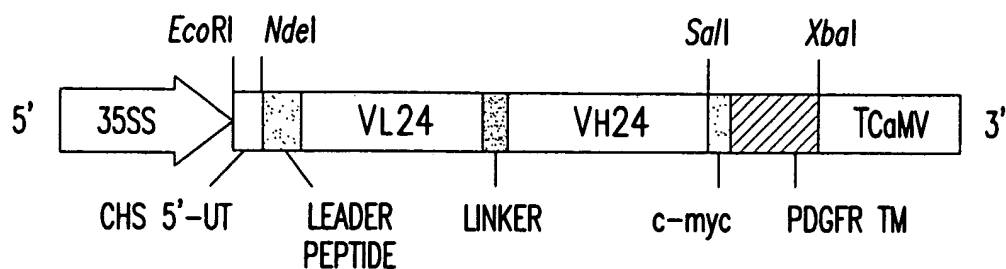


FIG.29



# REPLACEMENT SHEET

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*pscFv24-PDGFR*

FIG.30

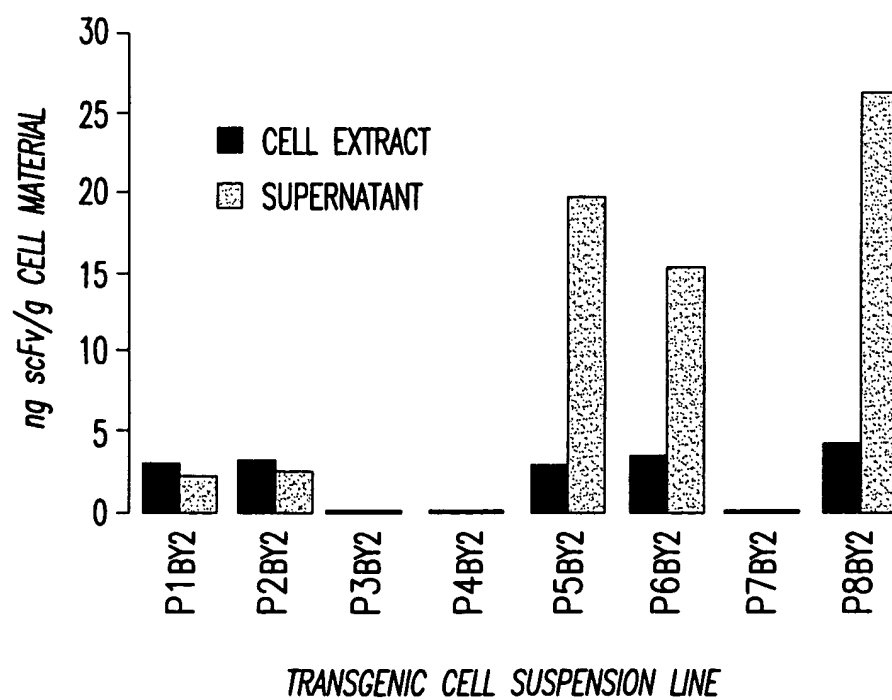


FIG.31

REPLACEMENT SHEET

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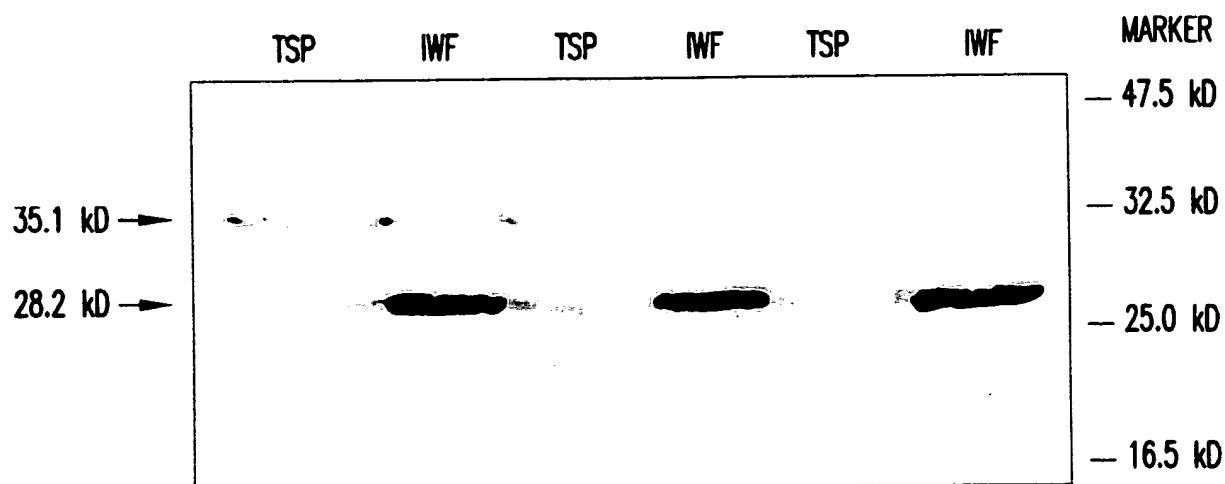


FIG.32A

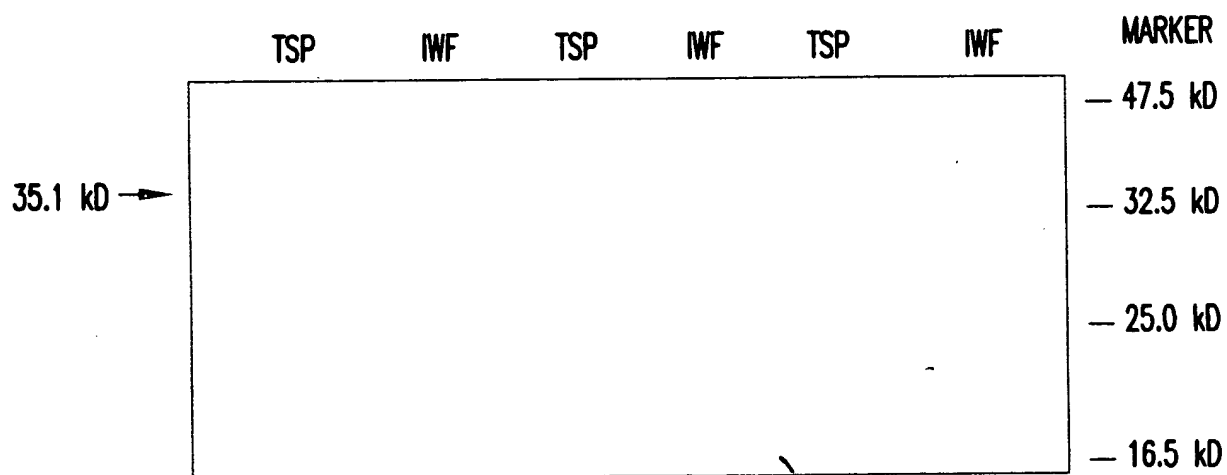


FIG.32B

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